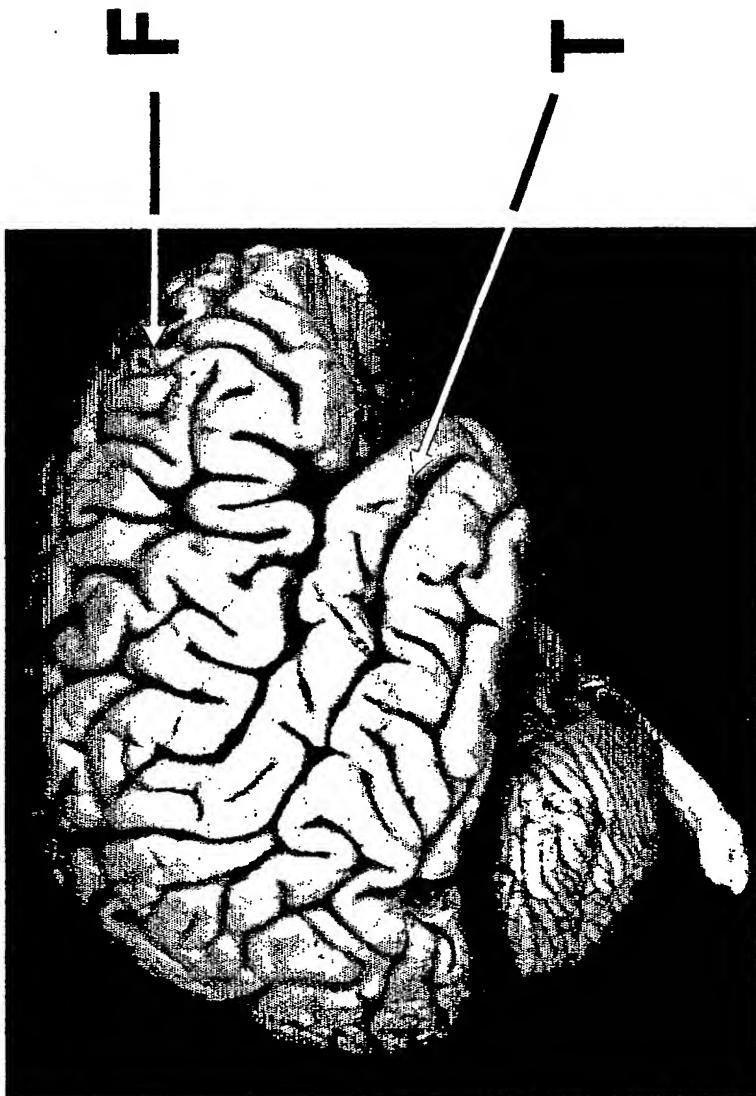


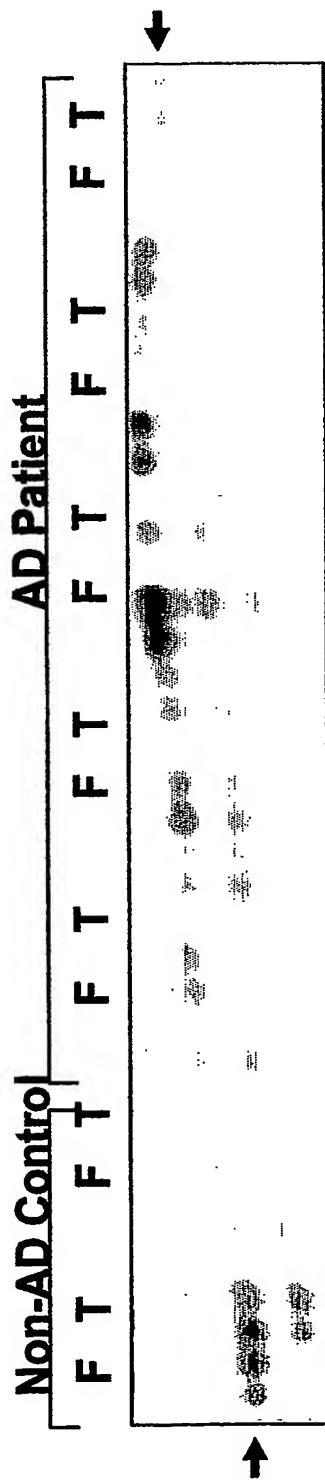
-1/25-

**Fig. 1: Identification of Genes Involved
in Alzheimer's Disease Pathology**



-2/25-

Fig. 2:Identification of differentially expressed genes in a fluorescence differential display screen



-3/25-

Figure 3: SEQ ID NO. 1

Length: 36 bp

1 AGTTAAGTTT CTTTGTAAAA CACTGATTTT TTCTCC

-4/25-

Fig. 4: Alignment of SEQ ID NO. 1 with human golgin-245 cDNA (GenBank accession number U41740)

-5/25-

Fig. 5: SEQ ID NO. 2: amino acid sequence of human golgin-245, splice variant 1

Length: 2228 aa

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRESGDTQS	FAQKLQLRVP	SVESLFRSPI	KESLFRSSSK	ESLVRTSSRE
101	SLNRLLDLDSS	TASFDP PSDM	DSEAEDLVGN	SDSLNKEQLI	QRLRRMERSL
151	SSYRGKYSEL	VTAYQMLQRE	KKKLQGILSQ	SQDKSLRRIA	ELREELQMDQ
201	QAKKHLQEEF	DASLEEKDQY	ISVLQTQVSL	LKQQLRNGPM	NVDVLKPLPQ
251	LEPQAEVFTK	EENPESDGEV	VVEDGTSVKT	LETLQQRVKR	QENLLKRCKE
301	TIQSHKEQCT	LLTSEKEALQ	EQLDERLQEL	EKIKDLHMAE	TKKLITQLRD
351	AKNLIEQLEQ	DKGMVIAETK	RQMHETLEMK	EEEIAQLRSR	IKQMTTQGEE
401	LREQKEKSER	AAFEELAKAL	STAQKTEEAR	RKLKAEMDEQ	IKTIEKTSEE
451	ERISLQQELS	RVKQEVVDVM	KKSSEEQIAK	LQKLHEKELA	RKEQELTKKL
501	QTREREFQEQ	MKVALEKSQS	EYLKISQEKE	QQESLALEEL	ELQKKAILTE
551	SENKLRLDLQQ	EAETYRTRIL	ELESSLEKSL	QENKNQSKDL	AVHLEAEKNK
601	HNKEITVMVE	KHKTELESLK	HQQDALWTEK	LQVLKQQYQT	EMEKLREKCE
651	QEKEPLLKDK	EIIIFQAHIEE	MNEKTLLEKLD	VKQTELESLS	SELSEVLKAR
701	HKLEEELSVL	KDQTDKMKQE	LEAKMDEQKN	HHQQQVDSII	KEHEVSIQRT
751	EKALKDQINQ	LELLLKERDK	HLKEHQAHVE	NLEADIKRSE	GELQQASAKL
801	DVFQSYQSAT	HEQTAKAYEEQ	LAQLQQKLLD	LETERILLTK	QVAEVEAQKK
851	DVCTELDAHK	IQVQDLMQQL	EKQNSEMEQK	VKS LTQVYES	KLEDGNKEQE
901	QTKQILVEKE	NMILQMREGQ	KKEIEILTQK	LSAKEDSIHI	LNEEYETKFK
951	NQEKKMEKVK	QAKAKEMQETL	KKKLLDQEAK	LKKELENTAL	ELSQKEKQFN
1001	AKMLEMAQAN	SAGISDAVSR	LETNQKEQIE	SLTEVHRREL	NDVISIWEKK
1051	LNQQAAEELQE	IHEIQLQEKE	QEVAELKQKI	LLFGCEKEEM	NKEITWLKEE
1101	GVKQDTTLNE	LQEQLKQKSA	HVNLSAQDET	KLKAHLEKLE	VDLNKSLKEN
1151	TFLQEQLVEL	KMLAEEDKRK	VSELTSKLKT	TDEEFQSLKS	SHEKSNSLE
1201	DKSLEFKKLS	EELAIQLDIC	CKKTEALLEA	KTNELINISS	SKTNAILSRI
1251	SHCQHRTTKV	KEALLIKTCT	VSELEAQLRQ	LTEEQNTLNI	SFQQATHQLE
1301	EKENQIKSMK	ADIESLVTEK	EALQKEGGNQ	QQAASEKESC	ITQLKKELSE
1351	NINAVTLMKE	ELKEKKVEIS	SLSKQLTDLN	VQLQNSISLS	EKEAAISSLR
1401	KQYDEEKCEL	LDQVQDLSFK	VDTLSKEKIS	ALEQVDDWSN	KFSEWKKAQ
1451	SRFTQHQNTV	KELQIQLLEK	SKEAYEKDEQ	INLLKEELDQ	QNKRFDCLKG
1501	EMEDDKSKME	KKESNLETEL	KSQTARIMEL	EDHITQKTI	IESLNEVLKN
1551	YNQQKDIIEHK	ELVQKLQHFQ	ELGEEKDNRV	KEAEKILTL	ENQVYSMKAЕ
1601	LETKKKELEH	VNL SVKSKEE	ELKALEDRLE	SESAAKLAE	KRKAEQKIAA
1651	IKKQLLSQME	EKEEYQKKGT	ESHLSELNTK	LQEREREVHI	LEEKLKSVES
1701	SQSETLIVPR	SAKNVAAYTE	QEEADSQGCV	QKTYEEKISV	LQRNLTEKEK
1751	LLQRVGQEKE	ETVSSHFEMR	CQYQERLIK	EHAEEAKQHED	QSMIGHLQEE
1801	LEEKNNKKYSL	IVAQHVEKEG	GKNNIQAQQN	LENVFDDVQK	TLQEKELTQ
1851	ILEQKIKELD	SCLVRQKEVH	RVEMEELTSK	YEKLQALQQM	DGRNKPTELL
1901	EENTEEKSKS	HLVQPKLLSN	MEAQHNDLEF	KLAGAEREKQ	KLGKEIVRLQ
1951	KDLRMLRKEH	QQELEILKKE	YDQEREKIK	QEQQEDLELKH	NSTLKQLMRE
2001	FNTQLAQKEQ	ELEMTEKTI	NKAQEVEAEL	LESHQEETNQ	LLKKIAEKDD
2051	DLKRTAKRYE	EILDAREEEM	TAKVRDLQTO	LEELQKKYQQ	KLEQEENPGN
2101	DNVTIMELQT	QLAQKTTLIS	DSKLKEQEFR	EQIHNLLEDRL	KKYEKNVYAT
2151	TVGTPYKGGN	LYHTDVSLLFG	EPTEFEYLRK	VLF EYMMGRE	TKTMAKVITT
2201	VLKFPDDQTO	KILEREDARL	MSWLRSSS		

-6/25-

**Fig. 6: SEQ ID NO. 3: nucleotide sequence of human
golgin-245 cDNA, splice variant 1**

Length: 7636 bp

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1  GCAACGAAGG TACCATGGCC GTTGTGTCG CCGCCGCGGC TCCCAGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CGGAAAGAAA GAGACGCGGC
101  GGCAGCGACG CCGACACCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
151  TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201  GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251  TTCTGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
301  AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351  TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAGAAATG AGGAGCAGGA
401  CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGTCA
451  GGTGACACAC AGTCTTTGC ACAGAAGCTC CAGCTCCGGG TGCCCTCCGT
501  GGAGTCTTTG TTTCGAAGTC CGATAAAAGGA ATCTCTATT CCGTCTTCTT
551  CTAAAGAGTC TTTGGTACGA ACATCTTCCA GAGAATCCCT GAATCGACTT
601  GACCTGGACA GTTCTACTGC CAGTTTTGAT CCACCCCTCG ATATGGATAG
651  CGAGGCTGAA GACTTGGTAG GGAATTCAAGA CAGTCTCAAC AAAGAACAGT
701  TGATTTCAGCG GTTGCAGAAGA ATGGAACGAA GCTTAAGTAG CTACAGGGGA
751  AAATATTCTG AGCTTGTAC AGCTTATCAG ATGCTTCAGA GAGAGAAGAA
801  AAAGCTACAA GGTATATTAA GTCAAGAGTCA GGATAAATCA CTTGGAGAGAA
851  TAGCAGAATT AAGAGAGGAG CTCCAAATGG ACCAGCAGGC AAAGAAACAT
901  CTGCAAGAGG AGTTTGATGC ATCTTTAGAG GAGAAAGATC AGTATATCAG
951  TGTTCTCCAA ACTCAGGTTT CTCTACTGAA ACAACGATTA CGAAATGGCC
1001  CGATGAATGT TGATGTTACTG AAACCACTTC CTCAGCTGGA ACCACAGGCT
1051  GAAGTCTTCA CTAAAGAAGA GAATCCAGAA AGTGTGAGG AGCCAGTAGT
1101  GGAAGATGGA ACTTCTGTAA AAACACTGGA AACACTCCAG CAAAGAGTGA
1151  AGCGTCAAGA GAACTACTT AAGCGTTGTA AGGAAACAAT TCAGTCACAT
1201  AAGGAACAAT GTACACTATT AACTAGTGAA AAAGAAGCTC TGCAAGAAC
1251  ACTGGATGAA AGACTTCAG AACTAGAAAA GATAAAAGGAC CTTCATATGG
1301  CCGAGAAGAC TAAACTTATC ACTCAGTTGC GTGATGCAAA GAACTTAATT
1351  GAACAGCTTG AACAAAGATAA GGGAAATGGTA ATCGCAGAGA CAAAAGTCA
1401  GATGCATGAA ACCCTGGAAA TGAAAGAAGA AGAAATTGCT CAACTCCGT
1451  GTCGCATCAA ACAGATGACT ACCCAGGGAG AGGAATTACG GGAACAGAAA
1501  GAAAAGTCCG AAAGAGCTGC TTTGAGGAA CTTGAAAAAG CTTTGAGTAC
1551  AGCCCCAAAAA ACAGAGGAAG CACGGAGAAA ACTGAAGGCA GAAATGGATG
1601  AACAAATAAA AACTATCGAA AAAACAAGTG AGGAGGAACG CATCAGTCTT
1651  CAACAGGAAT TAAGTCGGGT GAAACAGGAG GTTGTGATG TAATGAAAAA
1701  ATCCTCAGAA GAACAAATTG CTAAGCTACA GAAGCTTCAT GAAAAGGAGC
1751  TGGCCAGAAA AGAGCAGGAA CTGACCAAGA AGCTTCAGAC CCGAGAAAGG
1801  GAATTTCAAG AACAAATGAA AGTAGCTCTT GAAAAGAGTC AATCAGAATA
1851  TTTGAAGATC AGCCAAGAAA AAGAACAGCA AGAACATTTG GCCCTAGAAG
1901  AGTTAGAGTT GCAGAAAAAA GCAATCCTCA CAGAAAGTGA AAATAAAACTT
1951  CGGGACCTTC AGCAAGAAC AGAGACTTAC AGAAACTAGAA TTCTTGAATT
2001  GGAAAGTTCT TTGGAAAAAA GCTTACAAGA AAACAAAAAT CAGTCAAAAG
2051  ATTTGGCTGT TCATCTGAA GCTGAAAAAA ATAAGCACAA TAAGGAGATT
2101  ACAGTCATGG TTGAAAAAAC CAAGACAGAA TTGGAAAGCC TTAAGCATCA
2151  GCAGGATGCC CTTTGGACTG AAAAATCCTA AGTCTTAAAG CAACAAATATC
2201  AGACTGAAAT GGAAAAACTT AGGGAAAAGT GTGAACAAGA AAAAGAAACA
2251  TTGTTGAAAG ACAAAAGAGAT TATCTTCCAG GCCCACATAG AAGAAATGAA
2301  TGAAAAGACT TTAGAAAAGC TTGATGTGAA GCAAACAGAA CTAGAAATCAT
2351  TATCTTCTGA ACTGTCAAGA GTATTAAAAG CCCGTACAA ACTAGAAGAG
2401  GAACTTTCTG TTCTGAAAGA TCAAACAGAT AAAATGAAGC AGGAATTAGA
2451  GGCCAAGATG GATGAACAGA AAAATCATCA CCAGCAGCAA GTTGACAGTA

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-7/25-

2501 TCATTAAGA ACACGAGGT A TCTATCCAGA GGACTGAGAA GGCATTAAGA
2551 GATCAAATTA ATCAACTTGA GCTTCTCTTG AAGGAAAGGG ACAAGCATT
2601 GAAAGAGCAT CAGGCTCATG TAGAAAATTT AGAGGCAGAT ATTAAAAGGT
2651 CTGAAGGGGA ACTCCAGCAG GCATCTGCTA AGCTGGACGT TTTTCAGTCT
2701 TACCAGAGTG CCACACATGA GCAGACAAAA GCATATGAGG AACAGTTGGC
2751 CCAATTGCAG CAGAAGTTGT TGGATTGGA AACAGAAAGA ATTCTTCTTA
2801 CCAAACAGGT TGCTGAAGTT GAAGCACAAA AGAAAGATGT TTGTACTGAG
2851 TTAGATGCTC AAAAAATCCA GGTGCAGGAC TTAATGCAGC AACATTGAAAA
2901 ACAAATAGT GAAATGGAGC AAAAAGTAAA ATCTTAACC CAAGTCTATG
2951 AGTCCAAACT TGAAGATGGT AACAAAGAAC AGGAACAGAC AAAGCAAATC
3001 TTGGTGGAAA AGGAAAATAT GATTTACAA ATGAGAGAAC GACAGAAGAA
3051 AGAAATTGAG ATACTCACAC AGAAATTGTC AGCCAAGGAG GACAGTATT
3101 ATATTTGAA TGAGGAATAT GAAACCAAAT TAAAAAACCA AGAAAAAAAG
3151 ATGGAAAAAG TTAAGCAGAA AGCAAAGGAG ATGCAAGAAA CGTTAAAGAA
3201 AAAATTACTG GATCAGGAAG CCAAACCTAA GAAAGAGCTT GAAAATACTG
3251 CTCTAGAGCT TAGTCAGAAA GAAAAACAGT TTAATGCCA AATGCTGGAA
3301 ATGGCACAGG CTAACTCAGC TGGAATCAGT GATGCAGTGT CAAGACTGGA
3351 AACAAACCAA AAAGAACAAA TAGAAAGTCT TACTGAGGTT CATCGACGAG
3401 AACTCAATGA TGTCAATATCA ATCTGGGAAA AGAAACTTAA TCAGCAAGCT
3451 GAAGAACTTC AGGAAATACA TGAAATCCAA TTACAGGAAA AAGAACAAAGA
3501 GGTAGCAGAA CTGAAACAAA AGATCCTCCT ATTTGGGTGT GAAAAAGAAG
3551 AGATGAACAA GGAAATAACA TGGCTGAAGG AAGAAGGTGT TAAGCAGGAT
3601 ACAACATTAA ATGAATTACA GGAACAGTTA AAGCAGAAAGT CTGCCATGT
3651 GAATTCTCTT GCACAAGATG AAAACTAAACT GAAAGCTCAT CTTGAAAAGC
3701 TAGAGGTTGA CTTGAATAAG TCTCTGAAGG AAAATACTTT TCTTCAAGAG
3751 CAGCTAGTTG AACTGAAGAT GCTGGCAGAA GAAGATAAGC GGAAGGTTTC
3801 TGAGTTGACT AGCAAGTTGA AAACCACAGA TGAAGAATT CAGAGTTGA
3851 AATCTTCACA TGAAAAAAAGT AACAAAGCC TAGAGGACAA GAGCTTGGAA
3901 TTTAAAAAAC TGTCTGAGGA ACTAGCGATT CAGCTAGATA TTTGCTGTAA
3951 GAAAACCGAA GCCTTATTAG AAGCTAAAAC AAATGAGCTA ATCAACATTA
4001 GTAGTAGTAA AACTAATGCC ATTCTTTCTA GGATTCTCA TTGTCAGCAC
4051 CGTACAACTA AAGTTAAGGA GGCACGTGTT ATTAAAACCT GCACAGTTTC
4101 TGAATTAGAA GCACAACCTA GACAGTTGAC AGAGGAGCAA AATACACTAA
4151 ATATTTCTT TCAACAGGCT ACTCATCAGT TAGAAGAAAA AGAAAATCAA
4201 ATTAAGAGCA TGAAGGCTGA TATTGAAAGT CTTGTAACAG AAAAAGAAC
4251 CTTACAGAAG GAAGGAGGCA ATCAGCAACA GGCTGCTTCT GAAAAGGAGT
4301 CTTGTATAAC ACAGTTGAAG AAAGAGTTAT CTGAAAACAT CAATGCTGTC
4351 ACATTGATGA AAGAAGAGCT TAAAGAAAAA AAAGTTGAGA TTGAGCTCT
4401 TAGTAAACAA CTAACTGATT TGAATGTTCA GCTTAAAAT AGCATCAGCC
4451 TATCCGAAAA AGAACCGAGC ATTTCATCAC TAAGAAAGCA GTATGATGAA
4501 GAAAATGTG AATTGCTGGA TCAGGTGCAA GATTATCTT TTAAAGTTGA
4551 CACTCTGAGT AAAGAGAAAA TTTCTGCTCT TGAGCAGGTA GATGACTGGT
4601 CCAATAAATT CTCAGAATGG AAGAAGAAAG CACAGTCAAG ATTTACACAG
4651 CATCAAAACA CTGTTAAAGA ATTGCAGATC CAGCTTGAGT TAAAATCAA
4701 GGAAGCTTAT GAAAAGGATG AGCAGATAAA TTTATTGAAG GAAGAGCTTG
4751 ATCAGCAAAA TAAAAGATT GATTGTTAA AGGGTGAAAT GGAAGACGAC
4801 AAGAGCAAGA TGGAGAAAAA GGAGTCTAAT TTAGAAACAG AGTTAAAGTC
4851 TCAACACAGCA AGAATTATGG AATTAGAGGA CCATATTACC CAGAAAACCA
4901 TTGAAATAGA GTCTTAAAT GAAGTTCTTA AAAATTACAA TCAACAAAAG
4951 GATATTGAAC ACAAAAGAATT GGTCAGAAA CTTCAACATT TTCAAGAGTT
5001 AGGAGAAGAA AGGACAAACA GGGTTAAAGA AGCTGAAGAA AAAATCTTAA
5051 CACTTGAAAAA CCAAGTTAT TCCATGAAAG CTGAACCTGAA AACTAAGAAC
5101 AAAGAATTAG AACATGTGAA TTTAAGTGTG AAAAGCAAAG AGGAGGAGTT
5151 AAAGGCATTG GAAGATAGGC TTGAGTCAGA AAGTGCAGCA AAATTAGCAG
5201 AGTTGAAGAG AAAAGCTGAA CAAAAAATTG CTGCCATTAA GAAGCAGTTG

-8/25-

5251 TTATCTAAA TGGAAGAGAA AGAAGAACAG TATAAAAAG GTACAGAAAG
 5301 CCATTTGAGT GAGCTAAATA CAAAATTGCA GGAAAGAGAA AGGGAAAGTTC
 5351 ACATCTTGGG AGAAAAAATT AAGTCAGTGG AAAGTTCACCA GTCAGAAACA
 5401 TTAATTGTAC CCAGATCAGC AAAAAATGTG GCAGCATATA CTGAACAAAGA
 5451 AGAACAGAT TCCCAAGGCT GTGTGCAGAA GACATATGAA GAAAAAAATCA
 5501 GTGTTTACA AAGAAACTTA ACTGAAAAAG AAAAGCTATT GCAGAGGGTA
 5551 GGGCAGGAAA AAGAAGAGAC AGTTTCTTCT CATTGAAA TGCGATGCCA
 5601 ATACCAGGAG CGCTTAATAA AGCTAGAAC TGCTGAGGCA AAGCAACATG
 5651 AAGATCAAAG TATGATAGGT CATCTTCAAG AGGAGCTTGA AGAAAAAAAC
 5701 AAGAAATATT CCTTGATAGT AGCCCAGCAT GTGGAAAAAG AAGGAGGTAA
 5751 AAATAACATA CAGGCAAAGC AAAACTTGGG AAATGTGTT GACGACGTCC
 5801 AGAAAACCT CCAGGAGAAG GAACTAACCT GTCAGATTG GGAGCAAAAG
 5851 ATAAAAGAGC TGGATTCCCTG CTTAGTAAGA CAGAAAGAAG TACATAGAGT
 5901 TGAAATGGAA GAGTTGACT CAAAATATGA AAAATTACAG GCTTTACAAC
 5951 AGATGGATGG AAGAAATAAA CCCACAGAAC TTTTGGAGA AAACACTGAA
 6001 GAAAAGTCCA AATCACATT GGTCCAACCC AAATTGCTTA GTAACATGGA
 6051 AGCCCAGCAC AATGATCTGG AGTTTAAATT AGCCGGGGCA GAACGGGAGA
 6101 AACAGAAACT GGGCAAGGAG ATTGTTAGAT TGCAGAAAGA CCTTCGAATG
 6151 TTGAGAAAGG AGCATCAGCA AGAATTGGAA ATACTAAAGA AAGAATATGA
 6201 TCAAGAAAGG GAAGAGAAAA TCAACACAGGA GCAGGAAGAT CTTGAACCTGA
 6251 AGCACAATTC CACATTAAAA CAGCTGATGA GGGAGTTAA TACACAGCTG
 6301 GCACAAAAGG AACAAAGAGCT GGAAATGACC ATAAAAGAAA CTATCAATAA
 6351 GGCCCAGGAG GTGGAGGCTG AACTTTAGA AAGCCATCAA GAAGAGACAA
 6401 ATCAGTTACT TAAAAAAATT GCTGAGAAAG ATGATGATCT AAAACGAACA
 6451 GCCAAAAGAT ATGAAGAAAT CTTGATGCT CGTGAAGAAG AAATGACTGC
 6501 AAAAGTAAGG GACCTGCAGA CTCAACTTGA GGAGCTGCAG AAGAAATACC
 6551 AGCAAAAGCT AGAGCAGGAG GAGAACCCCTG GCAATGATAA TGTAACAATT
 6601 ATGGAGCTAC AGACACAGCT AGCACAGAAC ACGACTTAA TCAGTGATTC
 6651 GAAATTGAAA GAGCAAGAGT TCAGAGAAC GATTACAAT TTAGAAGACC
 6701 GTTTGAAGAA ATATGAAAAG AATGTATATG CAACAACTGT GGGGACACCT
 6751 TACAAAGGTG GCAATTGTA CCATACGGAT GTCTCACTCT TTGGAGAAC
 6801 TACCGAATTG GAGTATTG GAAAAGTGC TTTTGAGTAT ATGATGGTC
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 6951 ATGGCTCCGA TCTTCATCTT GAAGAAGAGT GACATTGGGT GACTGCTGCT
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 7151 TTTTCTTCAG TTTTCTCTTG GGAAGAGTT TATGTTGTTT AAAAGATATT
 7201 TTGATAACTT AACCTGCTT ATGGGCTTAC ATAATATTCC TTTCATCCAT
 7251 TCTTTTAAA GAACGGCTTA CCTTTCCTAT TTATTTTAG GGTGATTTTT
 7301 TAAAAAGACT TGTGCAATAC ATTTTGAGGT GAAACTTAGT GGATTTTTC
 7351 TGATAAATTG GAGCATTAA TTGACTATT TATTCAAGGTT GATCTGTTGA
 7401 ATATTGCTA AAGACCAAGTT CTTAAGCTA AGACATGTAA AAAATCCCAA
 7451 ATGGCAGTAC CTCATTGTT ACTTAGCTT TGTACTTATA TTTTCAGAG
 7501 GAAAAAACAC TACTGTAAAT TGTGAATAGC CAATACATAA CTGTATTGTA
 7551 TGCAAATCTG TGATTGTTGG CAGTGTATC TCTGAGAAC AGATAAATAA
 7601 AGTTTATTGTA CTATATAACC AAAAAAAAGA AAAAAAA

-9/25-

Fig. 7: SEQ ID NO. 4: amino acid sequence of human golgin-245, splice variant 2 (GenBank accession number Q13439)

Length: 2230 aa

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRESGDTQS	FAQKLQLRVP	SVESLFRSPI	KESLFRSSSK	ESLVRTSSRE
101	SLNRLLDLSS	TASFDP PSDM	DSEAEDLVGN	SDSLNKEQLI	QLRRMERSL
151	SSYRGKYSEL	VTAYQMLQRE	KKLQGILSQ	SQDKSLRRIA	ELREELQMDQ
201	QAKKHLQEEF	DASLEEKDQY	ISVLTQVSL	LKQRLRNGPM	NVDVLKPLPQ
251	LEPQAEVFTK	EENPESDGEV	VVEDGTSVKT	LETLQQRVKR	QENLLKRCKE
301	TIQSHKEQCT	LLTSEKEALQ	EQLDERLQEL	EKIKDLHMAE	KTKLITQLRD
351	AKNLIEQLEQ	DKGMVIAETK	RQMHEITLEMK	EEEIAQLRSR	IKQMTTQGEE
401	LREQKEKSER	AAFEELEKAL	STAQKTEEAR	RKLKAEMDEQ	IKTIEKTSEE
451	ERISLQQELS	RVKQEVDVM	KKSSEEQIAK	LQKLHEKELA	RKEQELTKKL
501	QTREREFSEQ	MKVALEKSQS	EYLKISQEKE	QQESLALEEL	ELQKKAILTE
551	SENKLRLDLQQ	EAETYRTRIL	ELESSLEKSL	QENKNQSKDL	AVHLEAEKNK
601	HNKEITVMVE	KHKTELES LK	HQQDALWTEK	LQVLKQQYQT	EMEKLREKCE
651	QEKE TLLKDK	EIIIFQAHIEE	MNEKTLEKLD	VKQTELESLS	SELSEVLKAR
701	HKLEEELSVL	KDQTDKMKQE	LEAKMDEQKN	HHQQQVDSII	KEHEVSIQRT
751	EKALKDQINQ	LELLLKERDK	HLKEHQAHVE	NLEADIKRSE	GELQQASAKL
801	DVFQSYQSAT	HEQT KAYEEQ	LAQLQQKLLD	LETERILLTK	QVAEVEAQKK
851	DVCTELDAHK	IQVQDLMQQL	EKQNSEMEQK	VKS LTQVYES	KLEDGNKEQE
901	QTKQILVEKE	NMILQMREGQ	KKEIEILTQK	LSAKEDSIHI	LNEEYETKFK
951	NQEKKMEKVK	QKAKEMQETL	KKKLLDQEAK	LKKELENTAL	ELSQKEKQFN
1001	AKMLEMAQAN	SAGISDAVSR	LETNQKEQIE	SLTEVHRREL	NDVISIWEKK
1051	LNQQAEELQE	IHEIQLQEKE	QEVAELKQKI	LLFGCEKEEM	NKEITWLKEE
1101	GVKQDTTLNE	LQEQLKQKSA	HVNLSAQDET	KLKAHLEKLE	VDLNKSLKEN
1151	TFLQEQLVEL	KMLAEEDKRK	VSELTSKLKT	TDEEFQSLKS	SHEKSNSKSL
1201	DKSLEFKKLS	EELAIQLDIC	CKKTEALLEA	KTNELINISS	SKTNAILSRI
1251	SHCQHRTTKV	KEALLIKTCT	VSELEAQLRQ	LTEEQNTLNI	SFQQATHQLE
1301	EKENQIKSMK	ADIESLVTEK	EALQKEGGNQ	QQAASEKESC	ITQLKKELSE
1351	NINAVTLMKE	ELKEKKVEIS	SLSKQLTDLN	VQLQNSISLS	EKEAAISSLR
1401	KQYDEEKCEL	LDQVQDLSFK	VDTLSKEKIS	ALEQVDDWSN	KFSEWKKKAQ
1451	SRFTQHQNTV	KELQIQLLELK	SKEAYEKDEQ	INLLKEELDQ	QNKRFDCLKG
1501	EMEDDKSKME	KKESNLETEL	KSQTARIMEL	EDHITQKTIE	IESLNEVLKN
1551	YNQQKDI EHK	ELVQKLQHFQ	ELGEEKDN RV	KEAEKILTL	ENQVYSMKA E
1601	LETKKKELEH	VNL SVKSKEE	ELKALEDRLE	SESAAKLAE L	KRKA EQKIAA
1651	IKKQLLSQME	EKEEYQKKGT	ESHLSELNTK	LQEREREVHI	LEEKLKSVES
1701	SQSETLIVPR	SAKNVAAYTE	QEEADSQGCV	QKTYEEKISV	LQRNLTEKEK
1751	LLQRVGQEKE	ETVSSH FEMR	CQYQERLIK L	EHAEAQHED	QSMIGHLQEE
1801	LEEKNNKKYSL	IVAQHVEKEG	GKNNI QAKQN	LENVFDDVQK	TLQEKELT CQ
1851	ILEQKIKELD	SCLVRQKEVH	RVEMEELTSK	YEKLQALQQM	DGRNKPTELL
1901	EENTEEKSKS	HLVQPKLLSN	MEAQHNDLE F	KLAGAEREKQ	KLGKEIVRLQ
1951	KDLRMLRKEH	QQELEILKKE	YDQERE EKIK	QE QEDLELKH	NSTLKQLMRE
2001	FNTQLAQKEQ	ELEM TI KETI	NKAQEVEAEL	LESHQEETNQ	LLKKIAEKDD
2051	DLKRTAKRYE	EILDAREEEM	TAKVRDLQTO	LEELQKKYQQ	KLEQEENPGN
2101	DNVTIMELQT	QLAQKTTLIS	DSKLKEQEFR	EQIHNL EDRL	KKYEKNVYAT
2151	TVGTPYKGGN	LYHTDVSLFG	EPTEFEYLRK	VLF EYMMGRE	TKTMAKVITT
2201	VLKF PDDQ TQ	KILEREDARL	MFTSPRSGIF		

-10/25-

Fig. 8: SEQ ID NO. 5: nucleotide sequence of human golgin-245 cDNA, splice variant 2 (GenBank accession number U41740)

Length: 7695 bp

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1  GCAACGAAGG TACCATGGCC GTTGTGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101  GGCGGCGACG CCGACACCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
151  TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201  GTGCCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251  TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
301  AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351  TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAAGAAATG AGGAGCAGGA
401  CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGTCA
451  GGTGACACAC AGTCTTTGAC ACAGAAAGCTC CAGCTCCGGG TGCCCTCCGT
501  GGAGTCTTTG TTTCGAAGTC CGATAAAAGGA ATCTCTATT CCGTCTTCTT
551  CTAAAGAGTC TTTGGTACGA ACATCTTCCA GAGAAATCCCT GAATCGACTT
601  GACCTGGACA GTTCTACTGC CAGTTTGAT CCACCCCTCTG ATATGGATAG
651  CGAGGCTGAA GACTTGGTAG GGAATTCAAGA CAGTCTCAAC AAAGAACAGT
701  TGATTTCAGCG GTTGCAGAAGA ATGGAACGAA GCTTAAGTAG CTACAGGGGA
751  AAATATTCTG AGCTTGTAC AGCTTATCAG ATGCTTCAGA GAGAGAAGAA
801  AAAGCTACAA GGTATATTAA GTCAGAGTC GGATAAAATCA CTTCGGAGAA
851  TAGCAGAATT AAGAGAGGAG CTCCAAATGG ACCAGCAGGC AAAGAACAT
901  CTGCAAGAGG AGTTTGATGC ATCTTTAGAG GAGAAAGATC AGTATATCAG
951  TGTCTCCAA ACTCAGGTTT CTCTACTGAA ACAACGATTA CGAAATGGCC
1001  CGATGAATGT TGATGTAATG AAACCACTTC CTCAGCTGGA ACCACAGGCT
1051  GAAGTCTTCA CTAAAGAAGA GAATCCAGAA AGTGTATGGAG AGCCAGTAGT
1101  GGAAGATGGA ACTTCTGTAA AAACACTGGA AACACTCCAG CAAAGAGTGA
1151  AGCGTCAAGA GAACCTACTT AAGCGTTGTA AGGAAACAAT TCAGTCACAT
1201  AAGGAACAAT GTACACTATT AACTAGTGAA AAAGAACAGTC TGCAAGAAC
1251  ACTGGATGAA AGACTTCAAG AACTAGAAAA GATAAAGGAC CTTCATATGG
1301  CCGAGAAGAC TAAACTTATC ACTCAGTTGC GTGATGCAAA GAACTTAATT
1351  GAACAGCTTG ACAAGATAA GGGAAATGGTA ATCGCAGAGA CAAAACGTCA
1401  GATGCATGAA ACCCTGGAAA TGAAAGAAGA AGAAATTGCT CAACTCCGTA
1451  GTCGCATCAA ACAGATGACT ACCCAGGGAG AGGAATTACG GGAACAGAAA
1501  GAAAAGTCCG AAAGAGCTGC TTTTGAGGAA CTTGAAAAG CTTTGAGTAC
1551  AGCCCAAAAA ACAGAGGAAG CACGGAGAAA ACTGAAGGCA GAAATGGATG
1601  AACAAATAAA AACTATCGAA AAAACAAGTG AGGAGGAACG CATCAGTCTT
1651  CAACAGGAAT TAAGTCGGGT GAAACAGGAG GTTGTGATG TAATGAAAAA
1701  ATCCTCAGAA GAACAAATTG CTAAGCTACA GAAGCTTCAT GAAAAGGAGC
1751  TGGCCAGAAA AGAGCAGGAA CTGACCAAGA AGCTTCAGAC CCGAGAAAGG
1801  GAATTTCAGG AACAAATGAA AGTAGCTCTT GAAAAGAGTC AATCAGAATA
1851  TTTGAAGATC AGCCAAGAAA AAGAACAGCA AGAATCTTG GCCCTAGAAG
1901  AGTTAGAGTT GCAGAAAAAA GCAATCCTCA CAGAAAGTGA AAATAAACTT
1951  CGGGACCTTC AGCAAGAAGC AGAGACTTAC AGAAACTAGAA TTCTTGAATT
2001  GGAAAGTTCT TTGGAAAAAA GCTTACAAGA AAACAAAAAT CAGTCAAAAG
2051  ATTTGGCTGT TCATCTGGAA GCTGAAAAAA ATAAGCACAA TAAGGAGATT
2101  ACAGTCATGG TTGAAAAAACAA CAAGACAGAA TTGGAAAGCC TTAAGCATCA
2151  GCAGGATGCC CTTTGGACTG AAAAACTCCA AGTCTTAAAG CAACAATATC
2201  AGACTGAAAT GGAAAAAACTT AGGGAAAAGT GTGAACAAGA AAAAGAAACA
2251  TTGTTGAAAG ACAAAAGAGAT TATCTTCCAG GCCCACATAG AAGAAATGAA
2301  TGAAAAGACT TTAGAAAAGC TTGATGTGAA GCAAACAGAA CTAGAATCAT
2351  TATCTTCTGA ACTGTCAGAA GTATTAAAAG CCCGTCACAA ACTAGAAGAG
2401  GAACTTTCTG TTCTGAAAGA TCAAACAGAT AAAATGAAGC AGGAATTAGA
2451  GGCCAAGATG GATGAACAGA AAAATCATCA CCAGCAGCAA GTTGACAGTA

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-11/25-

2501 TCATTAAAGA ACACGAGGTA TCTATCCAGA GGACTGAGAA GGCATTAAAA
2551 GATCAAATTA ATCAACTTGA GCTTCTCTTG AAGGAAAGGG ACAAGCATT
2601 GAAAGAGCAT CAGGCTCATG TAGAAAATTT AGAGGCAGAT ATTAAAAGGT
2651 CTGAAGGGGA ACTCCAGCAG GCATCTGCTA AGCTGGACGT TTTCAGTCT
2701 TACCAAGAGTG CCACACATGA GCAGACAAAA GCATATGAGG AACAGTTGGC
2751 CCAATTGCAG CAGAAGTTGT TGGATTGGA AACAGAAAGA ATTCTTCTTA
2801 CCAAACAGGT TGCTGAAGTT GAAGGCACAAA AGAAAGATGT TTGTACTGAG
2851 TTAGATGCTC ACAAAATCCA GGTGCAGGAC TTAATGCAGC AACTTGAAA
2901 ACAAAATAGT GAAATGGAGC AAAAGTAAA ATCTTTAACCA CAAGTCTATG
2951 AGTCCAAACT TGAAGATGGT AACAAAGAAC AGGAACAGAC AAAGCAAATC
3001 TTGGTGGAAA AGGAAAATAT GATTTACAA ATGAGAGAAG GACAGAAGAA
3051 AGAAAATTGAG ATACTCACAC AGAAAATTGTC AGCCAAGGGAG GACAGTATT
3101 ATATTTGAA TGAGGAATAT GAAACCAAAT TTAAAAACCA AGAAAAAAAAG
3151 ATGAAAAAAG TTAAGCAGAA AGCAAAGGAG ATGCAAGAAA CGTTAAAGAA
3201 AAAATTACTG GATCAGGAAG CCAAACCTAA GAAAGAGCTT GAAAATACTG
3251 CTCTAGAGCT TAGTCAGAAA GAAAACAGT TTAATGCCAA AATGCTGGAA
3301 ATGGCACAGG CTAACTCAGC TGGAAATCAGT GATGCAGTGT CAAGACTGG
3351 AACAAACCAA AAAGAACAAA TAGAAAGTCT TACTGAGGTT CATCGACGAG
3401 AACTCAATGA TGTCAATATCA ATCTGGAAA AGAAAACCTAA TCAGCAAGCT
3451 GAAGAACTTC AGGAAATACA TGAAATCCAA TTACAGGAAA AAGAACAAAGA
3501 GGTAGCAGAA CTGAAACAAA AGATCCTCCT ATTTGGGTGT GAAAAGAAAG
3551 AGATGAACAA GGAAATAACA TGGCTGAAGG AAGAAGGTGT TAAGCAGGAT
3601 ACAACATTAAT ATGAATTACA GGAACAGTTA AAGCAGAAAGT CTGCCCATGT
3651 GAATTCTCTT GCACAAAGATG AAAACTAAACT GAAAGCTCAT CTTGAAAAGC
3701 TAGAGGTTGA CTTGAATAAG TCTCTGAAGG AAAATACCTT TCTTCAAGAG
3751 CAGCTAGTTG AACTGAAGAT GCTGGCAGAA GAAGATAAGC GGAAGGTTTC
3801 TGAGTTGACT AGCAAGTTGA AAACCACAGA TGAAGAATTC CAGAGTTGA
3851 AATCTTCACA TGAAAAAAGT AACAAAAGCC TAGAGGACAA GAGCTTGGAA
3901 TTTAAAAAAC TGTCTGAGGA ACTAGCGATT CAGCTAGATA TTTGCTGTAA
3951 GAAAACCGAA GCCTTATTAG AAGCTAAAAC AAATGAGCTA ATCAACATTA
4001 GTAGTAGTAA AACTAATGCC ATTCTTCTA GGATTCTCA TTGTCAGCAC
4051 CGTACAACAA AAGTTAAGGA GGCACIGTTA ATTAAAACCTT GCACAGTTTC
4101 TGAATTAGAA GCACAACCTA GACAGTTGAC AGAGGAGCAA AATACACTAA
4151 ATATTTCTTT TCAACAGGCT ACTCATCAGT TAGAAGAAAA AGAAAATCAA
4201 ATTAAGAGCA TGAAGGCTGA TATTGAAAGT CTTGTAACAG AAAAAGAAC
4251 CTTACAGAAG GAAGGAGGCA ATCAGCAACA GGCTGCTTCT GAAAAGGAGT
4301 CTTGTATAAC ACAGTTGAAG AAAGAGTTAT CTGAAAACAT CAATGCTGTC
4351 ACATTGATGA AAGAAGAGCT TAAAGAAAA AAAGTTGAGA TTAGCAGTCT
4401 TAGTAAACAA CTAACGTATT TGAATGTTCA GCTTCAAAAT AGCATCAGCC
4451 TATCCAAAAA AGAACGAGCC ATTTCATCAC TAAGAAAGCA GTATGATGAA
4501 GAAAATGTG AATTGCTGGA TCAGGTGCAA GATTTATCTT TTAAAGTTGA
4551 CACTCTGAGT AAAGAGAAAA TTTCTGCTCT TGAGCAGGTA GATGACTGGT
4601 CCAATAAAATT CTCAGAATGG AAGAAGAAAG CACAGTCAG ATTACACAG
4651 CATCAAAACA CTGTTAAAGA ATTGCAGATC CAGCTTGAGT TAAAATCAA
4701 GGAAGCTTAT GAAAAGGATG AGCAGATAAA TTTATTGAAG GAAGAGCTTG
4751 ATCAGCAAAA TAAAAGATTT GATTGTTAA AGGGTGAAT GGAAGACGAC
4801 AAGAGCAAGA TGGGAGAAAAA GGAGTCTAAT TTAGAAACAG AGTAAAGTC
4851 TCAAACAGCA AGAATTATGG AATTAGAGGA CCATATTACC CAGAAAACTA
4901 TTGAAATAGA GTCCCTTAAAT GAAGTTCTTA AAAATTACAA TCAACAAAAG
4951 GATATTGAAC ACAAAAGATT GGTTCAGAAA CTTCAACATT TTCAAGAGTT
5001 AGGAGAAGAA AAGGACAACA GGGTTAAAGA AGCTGAAGAA AAAATCTTAA
5051 CACTTGAAAAA CCAAGTTTAT TCCATGAAAG CTGAACCTGA AACTAAGAAG
5101 AAAGAATTAG AACATGTGAA TTTAAGTGTG AAAAGCAAAG AGGAGGAGTT
5151 AAAGGCATTG GAAGATAGGC TTGAGTCAGA AAGTGCTGCA AAATTAGCAG

-12/25-

5201 AGTTGAAGAG AAAAGCTGAA CAAAAAATTG CTGCCATTAA GAAGCAGTTG
 5251 TTATCTCAA TGGAGAGAGA AGAAGAACAG TATAAAAAAG GTACAGAAAG
 5301 CCATTTGAGT GAGCTAAATA CAAAATTGCA GGAAAGAGAA AGGAAAGTTC
 5351 ACATCTTGGG AGAAAAACTT AAGTCAGTGG AAAGTTCACCA GTCAGAAACA
 5401 TTAATTGTAC CCAGATCAGC AAAAATGTG GCAGCATATA CTGAACAAGA
 5451 AGAACAGAT TCCCAGGCT GTGTGCAGAA GACATATGAA GAAAAAAATCA
 5501 GTGTTTACA AAGAAACTTAA ACTGAAAAAG AAAAGCTATT GCAGAGGGTA
 5551 GGGCAGGAAA AAGAACAGAC AGTTTCTTCT CATTGAAA TGCGATGCCA
 5601 ATACCAGGAG CGCTTAATAA AGCTAGAACAA TGCTGAGGCA AAGCAACATG
 5651 AAGATCAAAG TATGATAGGT CATCTTCAAG AGGAGCTTGA AGAAAAAAAC
 5701 AAGAAAATATT CCTTGATAGT AGCCCAGCAT GTGGAAAAAG AAGGAGGTAA
 5751 AAATAACATA CAGGCAAAGC AAAACTTGGG AAATGTGTT GACGACGTCC
 5801 AGAAAACCCCT CCAGGAGAAG GAACTAACCT GTTCAGATTG GGAGCAAAAG
 5851 ATAAAAGAGC TGGATTCTG CTTAGTAAGA CAGAAAGAAG TACATAGAGT
 5901 TGAAATGGAA GAGTTGACCT CAAAATATGA AAAATTACAG GCTTACAAC
 5951 AGATGGATGG AAGAAATAAA CCCACAGAAC TTTGGAAGA AAACACTGAA
 6001 GAAAAGTCCA AATCACATTG GGTCCAACCC AAATTGCTTA GTAACATGGG
 6051 AGCCCAGCAC AATGATCTGG AGTTTAAATT AGCCGGGGCA GAACGGGAGA
 6101 AACAGAAACT GGGCAAGGAG ATTGTTAGAT TGCAGAAAGA CCTTCGAATG
 6151 TTGAGAAAGG AGCATCAGCA AGAATTGGAA ATACTAAAGA AAGAATATGA
 6201 TCAAGAAAGG GAAGAGAAAA TCAAACAGGA GCAGGAAGAT CTTGAACCTGA
 6251 AGCACAATTG CACATTAAAA CAGCTGATGA GGGAGTTAA TACACAGCTG
 6301 GCACAAAAGG AACAAAGAGCT GGAAATGACC ATAAAAGAAA CTATCAATAA
 6351 GGCCCAGGAG GTGGAGGCTG AACTTTAGA AAGCCATCAA GAAGAGACAA
 6401 ATCAGTTACT TAAAAAAATT GCTGAGAAAG ATGATGATCT AAAACGAACA
 6451 GCCAAAAGAT ATGAAGAAAT CCTTGATGCT CGTGAAGAAG AAATGACTGC
 6501 AAAAGTAAGG GACCTGCAGA CTCAACTTGA GGAGCTGCAG AAGAAATACC
 6551 AGCAAAAGCT AGAGCAGGAG GAGAACCTG GCAATGATAA TGTAACAATT
 6601 ATGGAGCTAC AGACACAGCT AGCACAGAAG ACGACTTAA TCAGTGATTC
 6651 GAAATTGAAA GAGCAAGAGT TCAGAGAACAA GATTACAAT TTAGAAGACCC
 6701 GTTTGAAGAA ATATGAAAAG AATGTATATG CAACAACTGT GGGGACACCT
 6751 TACAAAGGTG GCAATTGTA CCATACGGAT GTCTCACTCT TTGGAGAACCC
 6801 TACCGAATTG GAGTATTGTC GAAAAGTGCT TTTTGAGTAT ATGATGGGT
 6851 GTGAGACTAA GACCATGGCA AAAGTTATAA CCACCGTACT GAAGTTCCCT
 6901 GATGATCAGA CTCAGAAAAT TTTGGAAGA GAAGATGCTC GGCTGATGTT
 6951 TACTTCACCT CGCAGTGGTA TCTTCTGAGT AAACCATCAG TCTGTGCTTA
 7001 GTTAACATGT GTCATGGCTC CGATCTTCAT CTTGAAGAAG AGTGACATTG
 7051 GGTGACTGCT GCTTGGAAAA CTGTCACAC TTGCTACTCT TTGAGAATGA
 7101 AGTTGTCATT CAGGGCCCCT CATGTAGCCA AAAGACCAAG AAAAATCTGG
 7151 CCCACAGATA AGTTGCAGAC TGCCTTAAAT ATAGATTAA TCAGTGGAGA
 7201 AATGGGTATA GTTTTTCTT CAGTTTCTC TTGGGAAGGA GTTTTATGTT
 7251 GTTAAAAGA TATTTGATA ACTTAACCTG CTTTATGGGC TTACATAATA
 7301 TTCTTTCAT CCATTCTTT TAAAGAACGG CTTACCTTC CTATTTATT
 7351 TTAGGGTGAT TTTTAAAAAA GACTTGTGCA ATACATTG AGGTGAAACT
 7401 TAGTGGATT TTTCTGATAA ATTAGAGCAT TTAATTGACT ATTATTATTCA
 7451 GGTGATCTG TTGAATATT GCTAAAGACC AGTTCTTAA GCTAAGACAT
 7501 GTAAAAAAATC CCAAATGGCA GTACCTCATT GTTTACTTAG CTTTGTACT
 7551 TATATTTTC AGAGGAAAAAA ACACACTGT AAATTGTGAA TAGCCAATAC
 7601 ATAACGTAT TGTATGCAA TCTGTGATTG TTGGCAGTGT CATCTCTGAG
 7651 AACAGATAA ATAAAGTTA TTTACTATAA AAAAAAAA AAAAG

-13/25-**Fig. 9: SEQ ID NO. 6: amino acid sequence of human golgin-245, splice variant 3****Length: 2250 aa**

1	MFKKLKQKIS	EEQQQLQQAL	APAQASSNSS	TPTRMRSRTS	SFTEQLDEGT
51	PNRENASTHA	SKSPDSVNGS	EPSIPQSGDT	QSFAQKLQLR	VPSVESLFRS
101	PIKESLFRSS	SKESLVRTSS	RESLNRLDLD	SSTASFDPPS	DMDSSEAEDLV
151	GNSDSLNKEQ	LIQRLRRMER	SLSSYRGKYS	ELVTAYQMLQ	REKKKLQGIL
201	SQSQDKSLLR	IAELREELQM	DQQAKKHLQE	EFDASLEEKD	QYISVLQTQV
251	SLLKQQLRNG	PMNVDVLKPL	PQLEPQAEVF	TKEENPESDG	EPVVVEDGTSV
301	KTLETLQQRV	KRQENLLKRC	KETIQSHKEQ	CTLLTSEKEA	LQEQLDERLQ
351	ELEKIKDLHM	AEKTKLITQL	RDAKNLIEQL	EQDKGMVIAE	TKRQMHETLE
401	MKEEEIAQQLR	SRIKQMTTQG	EELREQKEKS	ERAFAEELEK	ALSTAQKTEE
451	ARRKLKAEMD	EQIKTIEKTS	EEERISLQQE	LSRVKQEVVD	VMKKSSSEEQI
501	AKLQKLHEKE	LARKEQELTK	KLQTREREFQ	EQMVKALEKS	QSEYLKISQE
551	KEQQESLALE	ELELQKKAIL	TESENKLRLD	QQAETYRTR	ILELESSLEK
601	SLQENKNQSK	DLAVHLEAEK	NKHNKEITVM	VEKHKTELES	LKHQQDALWT
651	EKLQVLKQQY	QTEMEKLREK	CEQEKEETLLK	DKEIIIFQAH	EEMNEKTLEK
701	LDVKQTELES	LSELSEVLIK	ARHKLEEELS	VLKDQTDKMK	QELEAKMDEQ
751	KNHHQQQVDS	IIKEHEVSIQ	RTEKALKDQI	NQLELLLKER	DKHLKEHQAH
801	VENLEADIKR	SEGELQQASA	KLDVFQSYQS	ATHEQTKAYE	EQLAQLQQKL
851	LDLETERILL	TKQVAEVEAQ	KKDVTTELDA	HKIQVQDLMQ	QLEKQNSEME
901	QKVKSLTQVY	ESKLEDGNKE	QEQTQILVE	KENMILQMRE	GQKKEIEILT
951	QKLSAKEDSI	HILNEEYETK	FKNQEKKMEK	VKQKAKEMQE	TLKKKLLDQE
1001	AKLKKELENT	ALELSQKEKQ	FNAKMLEMAQ	ANSAGISDAV	SRLETNQKEQ
1051	IESLTEVHRR	ELNDVISIWE	KKLNQQAEEL	QEIHIEQLQE	KEQEVAELKQ
1101	KILLFGCEKE	EMNKEITWLK	EEGVVKQDTTL	NELQEQLKQK	SAHVNSLAQD
1151	ETKLKAHLEK	LEVDLNKSLLK	ENTFLQEQLV	ELKMLAEDDK	RKVSELTTSKL
1201	KTTDEEFQSL	KSSHEKSNSKS	LEDKSLEFKK	LSEELAIQLD	ICCKKTEALL
1251	EAKTNELINI	SSSKTNAILS	RISHCQHRTT	KVKEALLIKT	CTVSELEAQL
1301	RQLTEEQNTL	NISFQQATHQ	LEEKENQIKS	MKADIESLVT	EKEALQKEGG
1351	NQQQAASEKE	SCITQLKKEL	SENINAVTLM	KEELKEKKVE	ISLSQLTD
1401	LNVQLQNSIS	LSEKEAAISS	LRKQYDEEKC	ELLDQVQDLS	FKVDTLSKEK
1451	ISALEQVDDW	SNKFSEWKKK	AQSRFTQHQN	TVKELQIQL	LKSKEAYEKD
1501	EQINLLKEEL	DQQNKRFDCL	KGEMEDDKSK	MEKKESENLET	ELKSQTARIM
1551	ELEDHITQKT	IEIESLNEVL	KNYNQQKDI	HKELVQKLQH	FQELGEEKDN
1601	RVKEAEKIL	TLENQVYSMK	AELETKKEL	EHVNLSVSKSK	EEELKALEDR
1651	LESESAAKLA	ELKRKAEQKI	AAIKKQLLSQ	MEEKEEQYKK	GTEHLSLN
1701	TKLQEREREV	HILEEKLKSV	ESSQSETLIV	PRSAKNVAAY	TEQEEADSQG
1751	CVQKTYEEKI	SVLQRNLTEK	EKLLQRVGQE	KEETVSSHFE	MRCQYQERLI
1801	KLEHAEAKQH	EDQSMIGHLQ	EELEEKKNKY	SLIVAQHVEK	EGGKNNIQAK
1851	QNLENVFDDV	QKTLQEKELT	CQILEQKIKE	LDSCLVRQKE	VHRVEMEELT
1901	SKYEKLQALQ	QMDGRNKPT	LLEENTEEKS	KSHLVQPKLL	SNMEAQHNDL
1951	EFKLAGAERE	KQKLGKEIVR	LQKDLRMLRK	EHQQELEILK	KEYDQEREELK
2001	IKQEQEDLEL	KHINSTLQQLM	REFNTQLAQK	EQELEMTEKE	TINKAQEV
2051	ELLESHQEET	NQLLKKIAEK	DDDLKRTAKR	YEEILDAREE	EMTAKVRDLQ
2101	TQLEELQKKY	QQKLEQEENP	GNDNVTIMEL	QTQLAQKTTL	ISDSKLKEQE
2151	FREQIHNLED	RLKKYEKNVY	ATTVGTPYKG	GNLYHTDVSL	FGEPTEFY
2201	RKVLFEYMMG	RETKTMAKVI	TTVLKFPDDQ	TQKILEREDA	RLMSWLRSSS

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-14/25-

Fig. 10: SEQ ID NO. 7: nucleotide sequence of human golgin-245 cDNA, splice variant 3

Length: 7743 bp

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1  GCAACGAAGG TACCATGGCC GTTGTGTCG CCGCCGCGGC TCCCGGGGCT
51  GGATGGGGGG CCGAGGCCAG CCAGTGGCAC CCGGAAGAAA GAGACGCGGC
101  GGCGCGACG CCGACACCCT CAGGACCGAGT GTCCGGACTT GCCCACAGCC
151  TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201  GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCCTCAGGT
251  TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
301  AAGAAAAGA TCAGGGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351  TGCTCAGGCG TCCTCCAATT CTTCAACACC ACAAAGAATG AGGAGCAGGA
401  CATTTCTATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGAAT
451  GCATCTACTC ATGCCTCGAA ATCTCCTGAC AGTGTAAATG GAAGTGAACC
501  AAGCATTCCCT CAGTCAGGTG ACACACAGTC TTTTGCACAG AAGCTCCAGC
551  TCCGGGTGCC CTCCGTGGAG TCTTTGTTTC GAAGTCCGAT AAAGGAATCT
601  CTATTCCGGT CTTCTTCTAA AGAGTCTTG GTACGAACAT CTTCCAGAGA
651  ATCCCTGAAT CGACTTGACC TGGACAGTTC TACTGCCAGT TTTGATCCAC
701  CCTCTGATAT GGATAGCGAG GCTGAAGACT TGTTAGGGAA TTCAGACAGT
751  CTCAACAAAG AACAGTTGAT TCAGCGTTG CGAAGAATGG AACGAAGCTT
801  AAGTAGCTAC AGGGGAAAAT ATTCTGAGCT TGTTACAGCT TATCAGATGC
851  TTCAGAGAGA GAAGAAAAAG CTACAAGGTA TATTAAGTCA GAGTCAGGAT
901  AAATCACTTC GGAGAATAGC AGAATTAAGA GAGGAGCTCC AAATGGACCA
951  GCAGGCAAAG AAACATCTGC AAGAGGAGTT TGATGCATCT TTAGAGGAGA
1001  AAGATCAGTA TATCAGTGT TCTCAAACTC AGGTTCTCT ACTGAAACAA
1051  CGATTACGAA ATGGCCCGAT GAATGTTGAT GTACTGAAAC CACTTCCTCA
1101  GCTGGAACCA CAGGCTGAAG TCTTCACTAA AGAAGAGAAAT CCAGAAAGTG
1151  ATGGAGAGCC AGTAGTGGAA GATGGAACCTT CTGTAAAAAC ACTGGAAACA
1201  CTCCAGCAAA GAGTGAAGCG TCAAGAGAAC CTACTTAAGC GTTGTAAAGGA
1251  AACAAATTCAAG TCACATAAGG ACAATGTAC ACTATTAACT AGTAAAAAG
1301  AAGCTCTGCA AGAACAACTG GATGAAAGAC TTCAAGAACT AGAAAAGATA
1351  AAGGACCTTC ATATGGCCGA GAAGACTAAA CTTATCACTC AGTTGCGTGA
1401  TGCAAAGAAC TTAATTGAAC AGCTTGAACA AGATAAGGGA ATGGTAATCG
1451  CAGAGACAAA ACGTCAGATG CATGAAACCC TGGAAATGAA AGAAGAAGAA
1501  ATTGCTCAAC TCCGTAGTCG CATCAAACAG ATGACTACCC AGGGAGAGGA
1551  ATTACGGGAA CAGAAAGAAA AGTCCGAAAG AGCTGCTTTT GAGGAACCTG
1601  AAAAAGCTTT GAGTACAGCC CAAAAAACAG AGGAAGCACG GAGAAAAGTG
1651  AAGGCAGAAA TGGATGAACA AATAAAAAC ATCGAAAAAA CAAGTGAGGA
1701  GGAACGCATC AGTCTTCAAC AGGAATTAAAG TCGGGTGAAA CAGGAGGTTG
1751  TTGATGTAAT GAAAAAATCC TCAGAAGAAC AAATTGCTAA GCTACAGAAG
1801  CTTCATGAAA AGGAGCTGGC CAGAAAAGAG CAGGAACTGA CCAAGAAGCT
1851  TCAGACCCGA GAAAGGGAAT TTCAGGAACA AATGAAAGTA GCTCTTGAAA
1901  AGAGTCAATC AGAATATTG AAGATCAGCC AAGAAAAAGA ACAGCAAGAA
1951  TCTTGGCCC TAGAAGAGTT AGAGTTGCAG AAAAAAGCAA TCCTCACAGA
2001  AAGTAAAAT AAACCTCGGG ACCTTCAGCA AGAAGCAGAG ACTTACAGAA
2051  CTAGAATTCT TGAATTGGAA AGTTCTTTGG AAAAAAGCTT ACAAGAAAAC
2101  AAAAATCAGT CAAAAGATT GGCTGTTCAT CTGGAGCTG AAAAAAATAA
2151  GCACAATAAG GAGATTACAG TCATGGTTGA AAAACACAAG ACAGAATTGG
2201  AAAGCCTTAA GCATCAGCAG GATGCCCTT GGACTGAAAA ACTCCAAGTC
2251  TTAAAGCAAC AATATCAGAC TGAAATGGAA AAACCTAGGG AAAAGTGTGA
2301  ACAAGAAAAA GAAACATTGT TGAAAGACAA AGAGATTATC TTCCAGGCC
2351  ACATAGAAGA AATGAATGAA AAGACTTTAG AAAAGCTGTA TGTGAAGCAA
2401  ACAGAACTAG AATCATTATC TTCTGAACTG TCAGAAGTAT TAAAAGCCCG
2451  TCACAAACTA GAAGAGGAAC TTTCTGTTCT GAAAGATCAA ACAGATAAAA
2501  TGAAGCAGGA ATTAGAGGCC AAGATGGATG AACAGAAAAA TCATCACCAG

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-15/25-

2551 CAGCAAGTTG ACAGTATCAT TAAAGAACAC GAGGTATCTA TCCAGAGGAC
 2601 TGAGAAGGCA TAAAGGATC AAATTAATCA ACTTGAGCTT CTCTTGAGG
 2651 AAAGGGACAA GCATTGAAA GAGCATCAGG CTCATGTAGA AAATTTAGAG
 2701 GCAGATATTA AAAGGTCTGA AGGGGAACCT CAGCAGGCAT CTGCTAAGCT
 2751 GGACGTTTT CAGTCTTACC AGAGTGCCAC ACATGAGCAG ACAAAAGCAT
 2801 ATGAGGAACA GTTGGCCAA TTGCAGCAGA AGTTGTTGGA TTTGGAAACA
 2851 GAAAGAACATC TTCTTACCAA ACAGGTGCT GAAGTTGAAG CACAAAAGAA
 2901 AGATGTTGT ACTGAGTTAG ATGCTCACAA AATCCAGGTG CAGGACTAA
 2951 TGCAGCACT TGAAAAACAA AATAGTGAA TGGAGCAAA AGTAAAATCT
 3001 TTAACCCAAG TCTATGAGTC CAAACTGAA GATGGTAACA AAGAACAGGA
 3051 ACAGACAAAG CAAATCTTGG TGGAAAAGGA AAATATGATT TTACAAATGA
 3101 GAGAAGGACA GAAGAAAGAA ATTGAGATAC TCACACAGAA ATTGTCAGCC
 3151 AAGGAGGACA GTATTCATAT TTTGAATGAG GAATATGAAA CCAAATTAA
 3201 AAACCAAGAA AAAAGATGG AAAAGTTAA GCAGAAAGCA AAGGAGATGC
 3251 AAGAAACGTT AAAGAAAAAA TTACTGGATC AGGAAGCCAA ACTTAAGAAA
 3301 GAGCTTGAAA ATACTGCTCT AGAGCTAGT CAGAAAGAAA AACAGTTAA
 3351 TGCCAAAATG CTGGAAATGG CACAGGCTAA CTCAGCTGGA ATCAGTGATG
 3401 CAGTGTCAAG ACTGGAAACA ACCAAAAAG ACAAATAGA AAGTCTTACT
 3451 GAGGTTCATC GACGAGAACT CAATGATGTC ATATCAATCT GGGAAAAGAA
 3501 ACTTAATCAG CAAGCTGAAG AACTTCAGGA AATACATGAA ATCCAATTAC
 3551 AGGAAAAAGA ACAAGAGGTA GCAGAACTGA AACAAAAGAT CCTCCTATT
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 3651 AGGTGTTAAG CAGGATACAA CATTAAATGA ATTACAGGAA CAGTTAAAGC
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 3751 GCTCATCTTG AAAAGCTAGA GGTTGACTTG ATAAGTCTC TGAAGGAAA
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 3851 ATAAGCGGAA GGTTCTGAG TTGACTAGCA AGTTGAAAAC CACAGATGAA
 3901 GAATTCCAGA GTTGAAATC TTCACATGAA AAAAGTAACA AAAGCCTAGA
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 4101 TTCTCATTTG CAGCACCGTA CAACTAAAGT TAAGGAGGCA CTGTTAATT
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 4201 GAGCAAAATA CACTAAATAT TTCTTTCAA CAGGCTACTC ATCAGTTAGA
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 4351 GCTCTGAAA AGGAGTCTTG TATAACACAG TTGAAGAAAG AGTTATCTGA
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 5151 ACTTGAAACT AAGAAGAAAG AATTAGAAC A TGTGAATTAGT GTGTGAAAA
 5201 GCAAAAGAGGA GGAGTTAAAG GCATTGGAAG ATAGGCTTGA GTCAAGAAAGT

-16/25-

5251 GCTGCAAAAT TAGCAGAGTT GAAGAGAAAA GCTGAACAAA AAATTGCTGC
 5301 CATTAAAGAAG CAGTTGTTAT CTCAAATGGA AGAGAAAGAA GAACAGTATA
 5351 AAAAAGGTAC AGAAAGCCAT TTGAGTGGAC TAAATACAAA ATTGCAGGAA
 5401 AGAGAAAGGG AAGTTCACAT CTTGGAAGAA AAACCTTAAGT CAGTGGAAAG
 5451 TTCACAGTCA GAAACATTAA TTGTACCCAG ATCAGCAAA AATGTGGCAG
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 5701 GAGGCAAAGC AACATGAAGA TCAAAGTATG ATAGGTATC TTCAAGAGGA
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 6101 TGCTTAGTAA CATGGAAGCC CAGCACAATG ATCTGGAGTT TAAATTAGCC
 6151 GGGCAGAAC GGGAGAAACA GAAACTGGC AAGGAGATTG TTAGATTGCA
 6201 GAAAGACCTT CGAATGTTGA GAAAGGAGCA TCAGCAAGAA TTGGAAATAC
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 6301 GAAGATCTTG AACTGAAGCA CAATTCCACA TTAAAACAGC TGATGAGGG
 6351 GTTTAATACA CAGCTGGCAC AAAAGGAACA AGAGCTGGAA ATGACCATAA
 6401 AAGAAACTAT CAATAAGGCC CAGGAGGTGG AGGCTGAAC TTTAGAAAGC
 6451 CATCAAGAAG AGACAAATCA GTTACTTAAA AAAATTGCTG AGAAAGATGA
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 6551 AAGAAGAAAT GACTGAAAAA GTAAGGGACC TGCAGACTCA ACTTGAGGAG
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 7051 CATCAGTCTG TGCTTAGTTA ACATGTGTCA TGGCTCCGAT CTTCATCTTG
 7101 AAGAAGAGTG ACATTGGGTG ACTGCTGCTT GAAAAGACTGT CCACACTTGC
 7151 TACTCTTGA GAATGAAGTT GTCATTCAAGG GCCCTCATG TAGCCAAAG
 7201 ACCAAGAAAA ATCTGGCCCA CAGATAAGTT GCAGACTGCC TTTAAAATAG
 7251 ATTTTATCAG TGGAGAAATG GTGATAGTT TTTCTTCAGT TTTCTCTTGG
 7301 GAAGAGTTT ATGTTGTTA AAAGATATT TGATAACTTA ACCTGCTTTA
 7351 TGGGCTTACA TAATATTCTT TTCATCCATT CTTTTAAAG AACGGCTTAC
 7401 CTTTCCTATT TATTTTAAAG GTGATTTTT AAAAAGACTT GTGCAATACA
 7451 TTTTGAGGTG AAACCTTAGTG GATTTTTCT GATAAATTAG AGCATTAAAT
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 7551 TTTAAGCTAA GACATGTAAA AAATCCAAA TGGCAGTACC TCATTGTTTA
 7601 CTTAGCTTT GTACTTATAT TTTTCAGAGG AAAAACACT ACTGTAATT
 7651 GTGAATAGCC AATACATAAC TGTATTGTAT GCAAATCTGT GATTGTTGGC
 7701 AGTGTCACTCTGAGAAACA GATAAATAAA GTTTATTAC TAT

-17/25-

Fig. 11: SEQ ID NO. 8: amino acid sequence of human golgin-245, splice variant 4

Length: 2252 aa

1 MFKKLKQKIS EEEQQQLQQAL APAQASSNSS TPTRMRSRTS SFTEQLDEGT
 51 PNRENASTHA SKSPDSVNGS EPSIPQSGDT QSFAQKLQLR VPSVESLFRS
 101 PIKESLFRSS SKESLVRTSS RESLNRLDD SSTASFDPPS DMDSEAEDLV
 151 GNSDSLNKEQ LIQRLRRMER SLSSYRGKYS ELVTAYQMLQ REKKKLQGIL
 201 SQSQDKSLRR IAEELREELQM DQQAKKHLQE EFDASLEEKD QYISVLQTQV
 251 SLLKQRLRNG PMNVDVLKPL PQLEPQAEVF TKEENPESDG EPVVEDGTSV
 301 KTLETLQQRV KRQENLLKRC KETIQSHKEQ CTLLTSEKEA LQEQLDERLQ
 351 ELEKIKDLHM AEKTKLITQL RDAKNLIEQL EQDKGMVIAE TKRQMHETLE
 401 MKEEEIAQQLR SRIKQMTTQG EELREQKEKS ERAAEELEK ALSTAQKTEE
 451 ARRKLKAEMD EQIKTIEKTS EERIISLQQE LSRVKQEVD VMKKSSEEQI
 501 AKLQKLHEKE LARKEQELTK KLQTREREFQ EQMKVALEKS QSEYLKISQE
 551 KEQQQESLALE ELELQKKAIL TESENKLRLD QQEAETYRTR ILELESSLEK
 601 SLQENKNQSK DLAVHLEAK NKNKEITVM VEKHKTELES LKHQQDALWT
 651 EKLQVLKQQY QTEMEKLREK CEQEKEETLLK DKEIIIFQAH EEMNEKTLEK
 701 LDVKQTELES LSSELSEVLK ARHKLEEELS VLKDQTDKMK QELEAKMDEQ
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 801 VENLEADIKR SEGELQQASA KLDVFQSYQS ATHEQTKAYE EQLAQLQQKL
 851 LDLETERILL TKQVAEVEAQ KKDVTTELDA HKIQVQDLMQ QLEKQNSEME
 901 QKVKSLTQVY ESKLEDGNKE QEQTQILVE KENMILQMRG GQKKEIEILT
 951 QKLSAKEDSI HILNEEYETK FKNQEKKMEK VKQKAKEMQE TLKKKLLDQE
 1001 AKLKKELENT ALELSQKEKQ FNAKMLEMAQ ANSAGISDAV SRLETNQKEQ
 1051 IESLTEVHRR ELNDVISIWE KKLNQQAEEL QEIEIQLQE KEQEVAELKQ
 1101 KILLFGCEKE EMNKEITWLK EEGVKQDTTL NELQEQLKQK SAHVNSLAQD
 1151 ETKLKAHLEK LEVDLNKSLK ENTFLQEQLV ELKMLAEDK RKVSELTSKL
 1201 KTTDEEFQSL KSSHEKSNSK LEDKSLEFKK LSEELAIQLD ICCKKTEALL
 1251 EAATNELLINI SSSKTNAILS RISHCQHRTT KVKEALLIKT CTVSELEAQL
 1301 RQLTEEQNTL NISFQQATHQ LEEKENQIKS MKADIESLVT EKEALQKEGG
 1351 NQQQAASEKE SCITQLKKEL SENINAVTLM KEELKEKKVE ISSLSKQLTD
 1401 LNVQLQNSIS LSEKEAAISS LRKQYDEEKC ELLDQVQDLS FKVDTLSKEK
 1451 ISALEQVDDW SNKFSEWKKK AQSRTFQHQV TVKELQIQLR LKSKEAYEKD
 1501 EQINLLKEEL DQQNKRFDCL KGEMEDDKSK MEKKESENLET ELKSQTARIM
 1551 ELEDHITQKT IEIESLNEVL KNYNQQKDI E HKELVQKLQH FQELGEEKDN
 1601 RVKEAEEKIL TLENQVYSMK AELETKKEL EHVNLSVKSK EEEALKALEDR
 1651 LESESAAKLA ELKRKAEQKI AAIKKQLLSQ MEEKEEQYKK GTESHLSLN
 1701 TKLQERERREV HILEEKLKSV ESSQSETLIV PRSAKNVAAY TEQEEADSQG
 1751 CVQKTYEEKI SVLQRNLTEK EKLLQRVGQE KEETVSSHFE MRCQYQERLI
 1801 KLEHAEAKQH EDQSMIGHLQ EEELEEKNNKY SLIVAQHVEK EGGKNNIQAK
 1851 QNLENVFDDV QKTLQEKELT CQILEQKIKI LDSCLVRQKE VHRVEMEELT
 1901 SKYEKLQALQ QMDGRNKPT LLEENTEEKS KSHLVQPKLL SNMEAQHNDL
 1951 EFKLAGAERE KQKLGKEIVR LQKDLRMLRK EHQQELEILK KEYDQEREELK
 2001 IKQEQQEDLEL KHNSTLQQLM REFNTQLAQK EQELEMTIKE TINKAQEVVA
 2051 ELLESHQEET NQLLKKIAEK DDDLKRTAKR YEEILDAREE EMTAKVRDLQ
 2101 TQLEELQKKY QQKLEQEEENP GNDNVTIMEL QTQLAQKTTL ISDSKLKEQE
 2151 FREQIHNLED RLKYYEKNVY ATTGVTPYKG GNLYHTDVSL FGEPTEFYEL
 2201 RKVLFEYMMG RETKTMAKVI TTVLKFPPDQ TQKILEREDA RLMFTSPRSG
 2251 IF

-18/25-

Fig. 12: SEQ ID NO. 9: nucleotide sequence of human golgin-245 cDNA, splice variant 4

Length: 7761 bp

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1  GCAACGAAGG TACCATGGCC GTTGTCTCG CCGCCGCGGC TCCCCGGGCT
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101  GGCGGCGACG CCGACACCCCT CAGGACGAGT GTCCGGACTT GCCCACAGCC
151  TCAAGGAGGA GACGGCGAGG CCCGGCCCCC GCTGTCCCTG GTGTAAAGAA
201  GTCGCCGTAG CCGTCGCGGC CGGGACTCCC CGGGCTCTCG CCCTTCAGGT
251  TTCGTTGACA CTCAGGACCG TACGTACGCT GCGCCATGTT CAAGAAACTG
301  AAGCAAAAGA TCAGCGAGGA GCAGCAGCAG CTCCAGCAGG CGCTGGCTCC
351  TGCTCAGGCG TCCTCCAATT CTTCAACACC AACAAAGAATG AGGAGCAGGA
401  CATCTTCATT TACAGAGCAA CTTGATGAAG GTACACCCAA TAGAGAGAAT
451  GCATCTACTC ATGCCTCGAA ATCTCCTGAC AGTGTAAATG GAAGTGAACC
501  AAGCATTCCCT CAGTCAGGTG ACACACAGTC TTTGCACAG AAGCTCCAGC
551  TCCGGGTGCC CTCCGTGGAG TCTTGTTC GAAGTCCGAT AAAGGAATCT
601  CTATTCCGGT CTTCTTCTAA AGAGTCTTG GTACGAACAT CTTCCAGAGA
651  ATCCCCTGAAT CGACTTGACC TGGACAGTTC TACTGCCAGT TTTGATCCAC
701  CCTCTGATAT GGATAGCGAG GCTGAAGACT TGGTAGGGAA TTCAGACAGT
751  CTCAACAAAG AACAGTTGAT TCAGCGGTTG CGAAGAAATGG AACGAAGCTT
801  AAGTAGCTAC AGGGGAAAAT ATTCTGAGCT TGTTACAGCT TATCAGATGC
851  TTCAGAGAGA GAAGAAAAAG CTACAAGGTA TATTAAGTCA GAGTCAGGAT
901  AAATCACTTC GGAGAAATAGC AGAATTAAGA GAGGAGCTCC AAATGGACCA
951  GCAGGCAAAG AAACATCTGC AAGAGGAGTT TGATGCATCT TTAGAGGAGA
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1451  CAGAGACAAA ACGTCAGATG CATGAAACCC TGAAATGAA AGAAGAAGAA
1501  ATTGCTCAAC TCCGTAGTCG CATCAAACAG ATGACTACCC AGGGAGAGGA
1551  ATTACGGGAA CAGAAAGAAA AGTCCGAAAG AGCTGCTTT GAGGAACCTG
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1651  AAGGCAGAAA TGGATGAACA AATAAAAACAT ATCGAAAAAA CAAGTGAGGA
1701  GGAACGCATC AGTCTTCAAC AGGAATTAAAG TCGGGTGAAA CAGGAGGTTG
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1851  TCAGACCCGA GAAAGGGAAT TTCAGGAACA AATGAAAGTA GCTCTTGAAA
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2351  ACATAGAAGA AATGAATGAA AAGACTTTAG AAAAGCTTGA TGTGAAGCAA
2401  ACAGAACTAG AATCATTATC TTCTGAACCT TCAGAAGTAT TAAAAGCCCG
2451  TCACAAACTA GAAGAGGAAC TTTCTGTTCT GAAAGATCAA ACAGATAAAA

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-19/25-

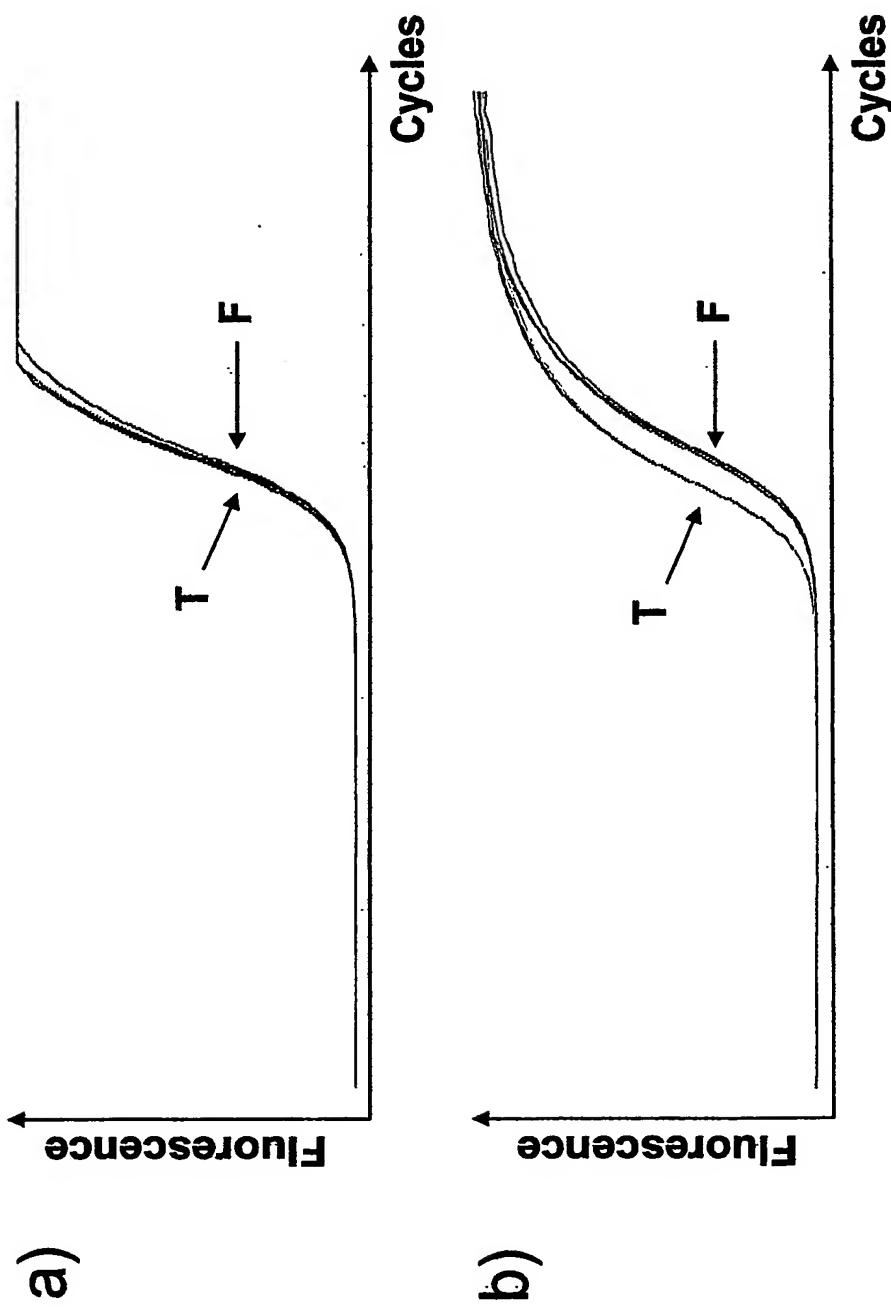
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 4951 ATTACCCAGA AAACTATTGA AATAGAGTCC TAAATGAAG TTCTTAAAAA
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 5151 ACTTGAAACT AAGAAGAAAG AATTAGAACA TGTGAATT A GTGTGAAAA

-20/25-

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5251	GCTGAAAAT	TAGCAGAGTT	GAAGAGAAAA	GCTGAACAAA	AAATTGCTGC
5301	CATTAAGAAG	CAGTTGTTAT	CTCAAATGGA	AGAGAAAGAA	GAACAGTATA
5351	AAAAAGGTAC	AGAAAGCCAT	TTGAGTGAGC	TAATACAAA	ATTGCAGGAA
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5451	TTCACAGTCA	GAAACATTAA	TTGTACCCAG	ATCAGAAAAA	AATGTGGCAG
5501	CATATACTGA	ACAAGAAGAA	GCAGATTCCC	AAGGCTGTGT	GCAGAAGACA
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5651	TTGAAATGCG	ATGCCAATAC	CAGGAGCGCT	TAATAAAGCT	AGAACATGCT
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6601	CTGCAGAAGA	AATACCAGCA	AAAGCTAGAG	CAGGAGGAGA	ACCCTGGCAA
6651	TGATAATGTA	ACAATTATGG	AGCTACAGAC	ACAGCTAGCA	CAGAAGACGA
6701	CTTTAATCAG	TGATTGCAA	TTGAAAGAGC	AAGAGTTCA	AGAACAGATT
6751	CACAATTTAG	AAGACCGTT	GAAGAAATAT	GAAAAGAATG	TATATGCAAC
6801	AACTGTGGGG	ACACCTTACA	AAGGTGGCAA	TTTGTACCAT	ACGGATGTCT
6851	CACTTTGG	AGAACCTTACC	GAATTTGAGT	ATTGCGAAA	AGTGTCTTTT
6901	GAGTATATGA	TGGGTCGTGA	GACTAAGACC	ATGGCAAAAG	TTATAACCAC
6951	CGTACTGAAG	TTCCCTGATG	ATCAGACTCA	GAAAATTG	GAAAGAGAAG
7001	ATGCTCGGCT	GATGTTACT	TCACCTCGCA	GTGGTATCTT	CTGAGTAAAC
7051	CATCAGTCTG	TGCTTAGTTA	ACATGTGTCA	TGGCTCCGAT	CTTCATCTTG
7101	AAGAAGAGTG	ACATTGGGTG	ACTGCTGCTT	GGAAAATCTG	CCACACTTGC
7151	TACTCTTGA	GAATGAAGTT	GTCATTCAAGG	GCCCCTCATG	TAGCCAAAG
7201	ACCAAGAAAA	ATCTGGCCCA	CAGATAAGTT	GCAGACTGCC	TTTAAAATAG
7251	ATTTTATCAG	TGGAGAAATG	GTGATAGTTT	TTTCTTCAGT	TTTCTCTTGG
7301	GAAGGAGTTT	TATGTTGTTT	AAAAGATATT	TTGATAACTT	AACCTGCTTT
7351	ATGGGCTTAC	ATAATATTCC	TTTCATCCAT	TCTTTTAA	GAACGGCTTA
7401	CCTTCCCTAT	TTATTTTAG	GGTGATTTTT	AAAAAAGACT	TGTGCAATAC
7451	ATTTTGAGGT	GAAACTTAGT	GGATTTTTC	TGATAAAATTA	GAGCATTAA
7501	TTGACTATTT	TATTCAGGTT	GATCTGTGA	ATATTTGCTA	AAGACCAGTT
7551	CTTTAAGCTA	AGACATGTAA	AAAATCCAA	ATGGCAGTAC	CTCATTGTTT
7601	ACTTAGCTTT	TGTACTTATA	TTTTCAGAG	GAAAAAACAC	TACTGTAAAT
7651	TGTGAATAGC	CAATACATAA	CTGTATTGTA	TGCAATCTG	TGATTGTTGG
7701	CAGTGTCATC	TCTGAGAAC	AGATAAAATAA	AGTTTATTTA	CTATAAAAAA
7751	AAAAAAAAAA	G			

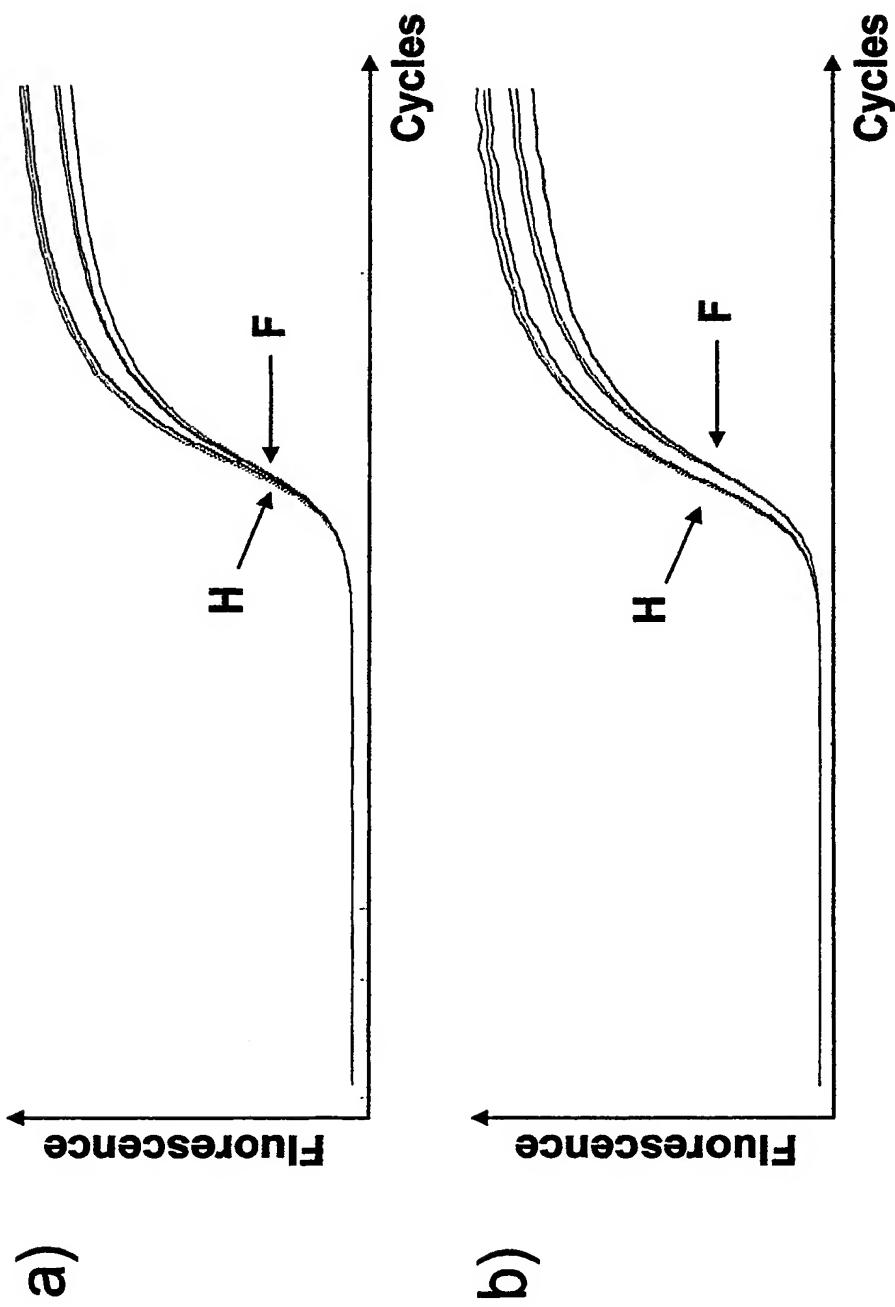
-21/25-

Fig. 13: Verification of differential expression of golgin-245 splice variant 1 and/or 3 by quantitative RT-PCR



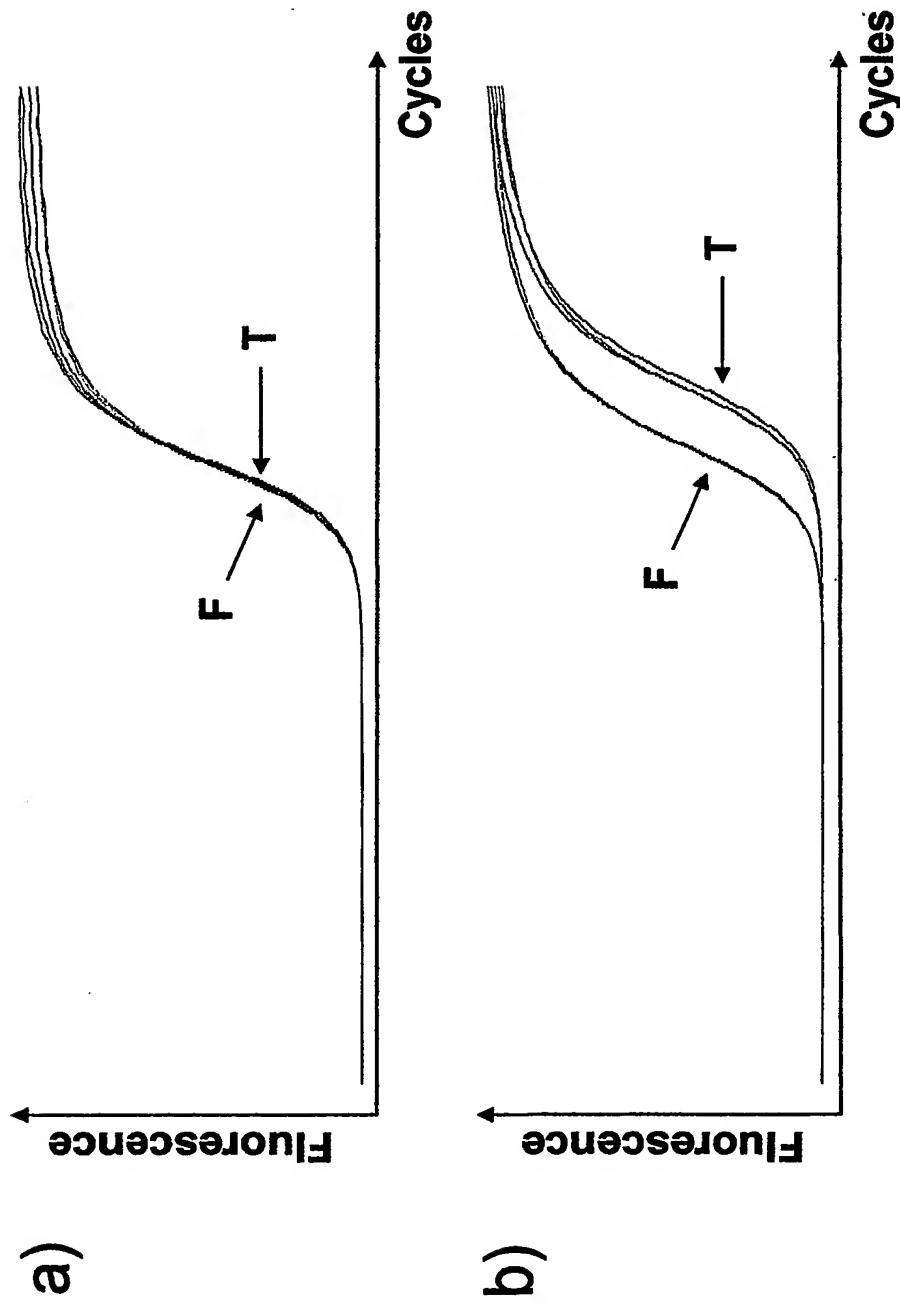
-22/25-

Fig. 14: Verification of differential expression of golgin-245 splice variant 1 and/or 3 by quantitative RT-PCR



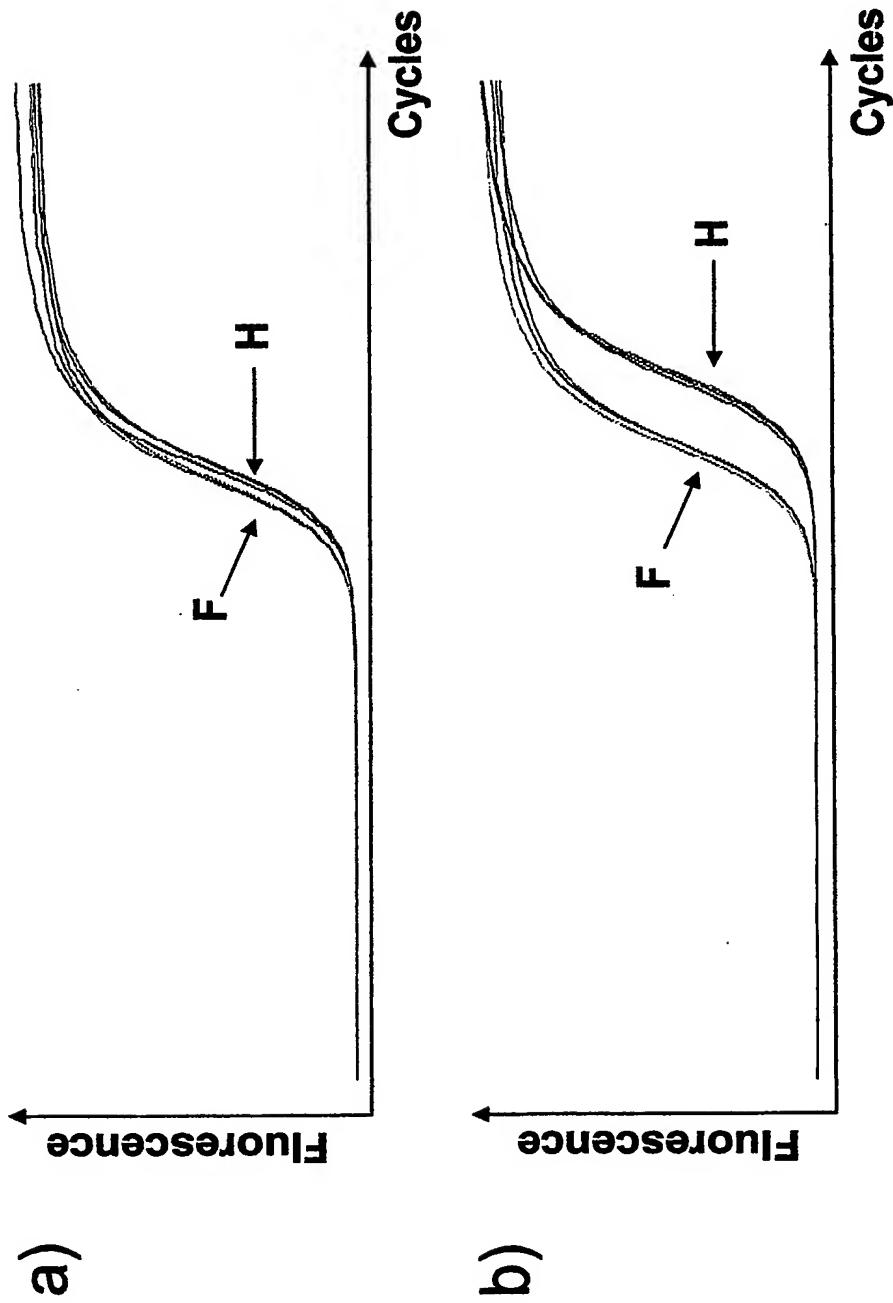
-23/25-

Fig. 15: Verification of differential expression of golgin-245 splice variant 2 and/or 4 by quantitative RT-PCR



-24/25 -

Fig. 16: Verification of differential expression of golgin-245 splice variant 2 and/or 4 by quantitative RT-PCR



-25/25-

Fig. 17: Images of the human cerebral cortex labeled with anti-golgin-245 monoclonal antibody and with DAPI

